

## **REMARKS/ARGUMENTS**

### **Sequence Listing**

The Examiner asserted that “[t]he sequences on Figs. 9 and 12 lack SEQ ID NO: Applicant is respectfully requested to identify the sequences on Figs. 9 and 12 or to submit a new Sequence Listing, which comprises said sequences.”

Applicant respectfully submits that 37 CFR § 1.1821(d) only requires the use of sequence identifiers in association with the written description and claims. The requirement does not extend to the drawing figures. Indeed, in the instant case, the addition of such identifiers would be wholly inappropriate in the context of the figures.

### **Amendments to the Specification**

Applicant has amended the specification to include section headings as noted by the Examiner. With regard to the possible introduction of new matter by the use of url's to describe websites, Applicant has amended the specification to indicate the state of such url's at the time of the instant application. Furthermore, Applicant respectfully submits that such url's merely describe the state of the art at the time of the invention.

### **Amendments to the Drawings**

Applicant has provided Replacement Drawing Sheets, which obviate the Examiner's objections regarding the blurriness and darkness of the original figures.

### **Claim Amendments**

1. Applicant has amended Claim 1 to replace “polynucleotides” with “a polynucleotide” as suggested by the Examiner.
2. Applicant has amended Claim 1 to replace “sequence identity of at least 50%,” with “sequence identity of at least 95%.” Support for the claim amendment can be found at least at page 10, paragraphs 2 and 3 of the original specification.

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3. Applicant has amended claim 1 to further recite “and said promoter providing a static defense and/or being inducible upon pathogen attack.” Support for the claim amendment can be found at least at page 4, lines 30-31, page 8, lines 17-20 and page 24, lines 12-14.

4. Applicant has added new claim 27, dependent from claim 1, and further reciting that “the promoter is active in the epidermis or the rhizodermis.” Support for new claim 27 can be found at least at page 23, lines 8-13 of the original specification.

5. Applicant has added new claim 28, dependent from claim 1, which further recites that the “promoter ensures expression in photosynthetically active tissues only.” Support for new claim 28 can be found at least at page 23, lines 14-20 of the original specification.

6. Applicant has amended claim 3 to recite “a vector comprising the recombinant nucleic acid molecule of claim 1.”

7. Applicant has amended other of the claims to address grammatical type issues and/or antecedent issues.

**Claim Rejections under 35 USC § 112, second paragraph**

The Examiner rejected claims 3-7 and 12-16 as allegedly indefinite. While not agreeing with the Examiner’s underlying basis for the rejection, Applicant has nonetheless, amended such claims to advance prosecution.

The rejections should be withdrawn.

**Claim Rejections under 35 USC § 112, first paragraph**

Claims 1-8 and 11-16 stand rejected as allegedly not reasonably enabling “a recombinant nucleic acid molecule comprising a polynucleotide encoding a fragment of SEQ ID NO: 2 or

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encoding a polypeptide having at least 50% [identity] to SEQ ID NO:2 and having beta-glucosidase activity.”

Applicant has amended claim 1 to delete element “(c)” and had further amended the claim to replace 50% with 95% thereby obviating the rejection. Applicant respectfully submits that in view of the state of the art and the instant disclosure, an ordinarily skilled artisan would be sufficiently enable to make make and use the claimed invention without undue experimentation.

The rejection should be withdrawn.

#### **Claim Rejections under 35 USC § 102**

1.) The Examiner rejected Claims 1-8 and 11-16 under 35 USC § 102(e) as allegedly being anticipated by Harper (US 7,109,033). More specifically, the Examiner asserted, “Harper teaches a recombinant nucleic acid/vector comprising a nucleotide sequence encoding a polypeptide that is 100% identical to Applicant's SEQ ID NO: 2 (see attached alignment of sequence) and having beta-glucosidase activity (see SEQ ID NO: 54 on Table 1; column 61) operably linked to regulatory sequences including a promoter region; transgenic plant/cell and host cells transformed with said vector or recombinant nucleic acid; and a method of transforming host cell/plant with said vector to produce transgenic plant having resistance against stress (see at least col. 4-5; paragraph bridging 13-14; col. 19-20, 29-34, and 43-49). Since the nucleic acid of Harper (SEQ ID NO: 54) is 100% identical to Applicant's SEQ ID NO: 1, the disease resistance activity is an inherent property to the Harper's SEQ ID NO: 54. Therefore, Harper teaches all claim limitations.”

Applicant has amended claim 1 to recite “a promoter operatively linked to said polynucleotide, said promoter being heterologous with respect to the polynucleotide and said promoter providing a static defense and/or being inducible upon pathogen attack,” and respectfully submits that Harper fails to explicitly or implicitly describe such features.

That is, Harper describes plant genes that are regulated in response to one or more abiotic stress conditions (See column 17, lines 4-5). As described at Col. 18, line 35 – Col. 19, line 3,

abiotic stressors are defined as stressors of the type, for example, resulting from salt stress, drought stress, etc. Accordingly, Harper does not describe biotic stress and does not describe biotic stress caused by pathogens, and the like. More particularly, Harper does not describe promoters that provide static defense or inducible defense upon attack by pathogens. Accordingly, Harper fails to describe each and every element of amended claim 1 as is needed to support a rejection under 35 USC § 102.

The rejection should be withdrawn.

2.) The Examiner rejected Claims 1-8 and 11-16 under 35 USC 102(e) as allegedly anticipated by Duvick et al (US 6,433,249). More specifically, the Examiner asserted that Duvick describe an isolated gene encoding a polypeptide having beta glucosidase activity that is cloned into a plant expression vector comprising regulatory sequences, and methods of transforming a host cell and plants with said vector to produce transgenic plants having enhanced resistance to diseases and insects. The cited reference also teaches transformed plants and host cells expressing said polypeptide having beta glucosidase activity . Given that claim 1, part c encompasses "a fragment" of any size of SEQ ID NO: 2 having beta-glucosidase activity . Duvick et al discloses all claim limitations."

Applicant has amended claim 1 to delete "part (c)" and has further amended such claim to recite that the promoter is "operatively linked to said polynucleotide, said promoter being heterologous with respect to the polynucleotide and said promoter providing a static defense and/or being inducible upon pathogen attack," and respectfully submits that Duvick fails to explicitly or implicitly describe such features. Additionally, amended claim 1 further recites "a polynucleotide comprising a nucleotide sequence which encodes a polypeptide having a sequence identity of at least 95% to an amino acid sequence encoded by the polynucleotide of (a) or (b), wherein said polypeptide has R-glucosidase activity." However, as shown in Applicant's Appendix, results of GAP and BestFit sequence alignments of SEQ ID NO:1 of the claimed invention and SEQ ID NOS: 1 and 3 of Duvick set forth that there is less than 57% identity between the sequences. Similarly, the sequence alignment of SEQ ID NO: 2 of the claimed

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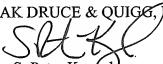
invention and SEQ ID NOS: 2 and 4 of Duvick illustrate an identity of below 50%. Accordingly, Applicant respectfully submits that Duvick further fails to disclose each and every element of amended claim 1 as required to support a rejection under 35 USC §102.

Accordingly, the rejection should be withdrawn.

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**Conclusion**

Applicants respectfully submit that the present application is in condition for allowance, which action is courteously requested. Please charge any shortage in fees due in connection with the filing of this paper, including Extension of Time fees to Deposit Account No. 14-1437. Please credit any excess fees to such deposit account.

Respectfully submitted,  
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Dated: May 19, 2008

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### **APPENDIX**

This appendix includes the following:

- 1.) Replacement Drawing Sheets; and,
- 2.) GAP (4) and BestFit (4) Sequence Alignment Comparisons.

attached Replacement Sheet and Annotated Sheet Showing Changes Made for consideration by the Examiner.

# GAP (Present Application SEQ ID NO 1 versus Duvick SEQ ID NO 1)

GAP of: Present application from: 1 to: 1683

readseq-55023\_tmp\_1 1683 bp

to: DUVICK from: 1 to: 1931

readseq-53826\_tmp\_1 1931 bp

Symbol comparison table: /applications/gcg/share/matrix/nwsgapdna.cmp  
CompCheck: 8760

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Length Weight:	3	Average Mismatch:	0.000
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Ratio:	4.711	Gaps:	7
Percent Similarity:	50.030	Percent Identity:	50.030

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. = 1

x May 16, 2008 19:06 ..

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      .
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      | | | | | | | | | | | | | | | | | | | | | |
43 ggtagagctagctttccaaaaggctttctctttggaactgcttcatcttc 92
      | | | | | | | | | | | | | | | | | | | | | |
251 caaagggactgggtccctctgacttcaccttcggtgccccacttcagc 300
      | | | | | | | | | | | | | | | | | | | | | |
93 ttatcagtacgaaggagcagtgatgaaggtgcgagaggacaaagcgtgt 142
      | | | | | | | | | | | | | | | | | | | | | |
301 gtaccaaatgaaggtgcttggaatgaagatggaaagggggaagcaact 350
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143 gggatcatttctccaacaggtttctcctcacagaatcagtgattctagcgac 192
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351 gggatcactcttgccacaatcatccggaaggatactggacgggagcaat 400
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193 ggaaacgttgccgttgatttctaccatcggtacaaggaagatattaagag 242
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401 tcagacattggagcggaattcgatatcatatgtacaaaacggacgtcagatt 450
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243 aatgaaggatataaacatggattcggttcggctttccattgcttggccac 292
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451 gctcaaggaaatggcgtagcgacatagatttctctatctcttggccca 500
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293 gagttctaccttatggcaaaagggatagaggagtttagtgaagaaggaatt 342
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501 gaatactgccgaagggaaccaagaaggagggtattaaccctgatggcatc 550
      | | | | | | | | | | | | | | | | | | | | | |
343 aagttttacaatgatgttattgatgaactcttagccaatgaaatcactcc 392
      | | | | | | | | | | | | | | | | | | | | | |
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[illegible]

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1398 tctacatcaccgagaaacgggaatcggggatgttgataccaagagacacct 1447  
1231 ctttatatgtacaatcctcacaatcgacacagagagattggagtacattga 1280  
1448 ctacccatggaggctgccttaaatgactacaaaaggctagattacatcca 1497  
1281 aggacatatccacgcgtattcatcaagccatccatgaagatggagtaagag 1330  
1498 gcgcacatcgctactcttaagggaatcaat...agacttgggatacaatg 1544  
1331 tggaagggttattacgtatggtcattgtcatagataaacttcagtggaacagt 1380  
1545 tcaaggctacttcgcttggctctctgctggacaactcttgaatggttgcc 1594  
1381 ggatattggtgtgagatatggttttatatcacattgattacaaagatgggct 1430  
1595 ggcttcaccggaacgttatggcattgtctacgtcgaccgcaacaataactg 1644  
1431 tagacgataccgaaaaatgtcggcgcttatggttgaaagagttcttga... 1477  
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1478 ..ggtttgatcaagaagacgattcttcgac..gtctaaagaaagaagaa 1523  
1695 cgaaaaagccacgacaagaagattctctacgccagcttaaaaaatcgggggcc 1744  
1524 gaaagagagctatgaaaaacagttattgcattctgttcaggacagctcaat 1573  
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1795 tttctctctttttctctgccacgagaggttctctggaggcatactctcca 1844  
1612 gttttggggagcttgttcgtttgtgtctgcgaactgttggttactctctgtt 1661  
1845 gcaccgtggctaataaacgcgtgtgttccaattcagctgcgccttgtcatgc 1894  
1662 cttcaaggagctataataatTga..... 1683  
1895 atcgaataataaagtgatgggtttccctgtttcaat 1931

## GAP (Present application SEQ ID NO 2 versus Duvich SEQ ID NO 2)

GAP of: Present application SEQ ID NO 2 from: 1 to: 560

readseq-64383\_tmp\_1 560 bp

to: DUVICH SEQ ID NO 2 from: 1 to: 566

readseq-34465\_tmp\_1 566 bp

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Length Weight:	2	Average Mismatch:	-2.248
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Ratio:	1.929	Gaps:	6
Percent Similarity:	52.988	Percent Identity:	44.024

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x May 16, 2008 18:50 ..

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      .
      .
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51 FTTRSARVGSQNGVQLSPSEIQ.RDWFPSPDFTFGAATSAYQIEGAVNE 99
      .| .| .| .| .| .| .| .| .| .| .| .| .| .|
41 GARGQSVNDHFSNRFPHRISDSDGNVAVDFYHRYKEDIKRMKDINMDSF 90
      :| :| :| :| .| .| .| .| .| .| .| .| .| .|
100 DGKGESNWDHFCNHHPERILDGNSNDIGANSYHMYKTDVRLLEKMGMDAY 149
      .| .| .| .| .| .| .| .| .| .| .| .| .| .|
91 RLSTIAWPRVLPYGRDRGVSEEGIKFYNDVIDELLANEITPLVTIFHWDI 140
      | | | | | :| :| :| .| .| .| .| .| .| .| .| .|
150 RFSISWPRILPKGTKEGGINPDGIKYYRNLINLLLENGIEPYVTIFHWDV 199
      .| .| .| .| .| .| .| .| .| .| .| .| .| .|
141 PQDLEDEYGGFLS...EQIIDDFRDYASLCFERFGDRVSLWCTMNEPVY 187
      || | | .| | | | .| :| :| :| .| .| .| .| .| .|
200 PQALEEKYGGFLDKSHKSIVEDYTYFAKVCFDNPGDKVKNWLTFNBPQTF 249
      .| .| .| .| .| .| .| .| .| .| .| .| .| .|
188 SVAGYDTGRKAPGRCSKYVNGASVAGMSGYEAYIVSHNMLLAHAEAVEVF 237
      .| .| .| .| | | | | .| .| .| .| .| .| .| .| .|
250 TSFSYGTGVFAPGRCSPLGLDCAYPGTGNSLVEPYTAGHNILLAHAEAVDLY 299
      .| .| .| .| .| .| .| .| .| .| .| .| .| .|
238 RKCDHIKNGQIGIAHNFLWYEPYDPSDDPDDVEGCNRAMDFMLGWHQHPTA 287
      | | .| :| :| .| .| .| .| .| .| .| .| .| .|
300 NKHYKRDDTRIGLAFDVMGRVPYGTSLFLDK.QAEBERSWDINLGWFLEPVV 348
      .| .| .| .| .| .| .| .| .| .| .| .| .| .|
288 CGDYPTMKKSVGDRLPSTPEQSKKLIGSCDYVGINYYSSLFVSKIKHV 337
      || | | .| :| :| | | | | .| .| .| .| .| .| .|
349 RGDYPPSMRSLARERLPFFKDEQKEKLAGSYNMLGLNYTTSRFSKNIDIS 398
      .| .| .| .| .| .| .| .| .| .| .| .| .| .|
338 DPTOPTWRTDQGVDMWMTKN.IDGKQIAKQGGSEWSFTYPTGLRNILKYVK 386
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399 PNYSFVLNITDDAYASQEVNGPDGKPIGPPMGNPWIMYMEGLKDLLMIMK 448
387 KTYGNPPILITENGYGEVAEQSQSLYMYNPSIDTERLEYIEGHIHAIHQ 436
    ||||| ||||| |:| . | | | .||:|: || : :.
449 NKYGNPPIYITENGIGDVKETPLPMEALNDYKRLDYIQRHIATLKES 498
437 IHEDGVRVEGYVWSLLDNFEWNSGYGVRYGLYYIDYKDGLRRYPKMSAL 486
    | : | |:|: ||||| |||. |: ||: |:| . || | ||
499 I.DLGSNVQGYFAWSLLDNFEWFAGFTERYGIVYVDRNNNCTRYMKESAK 547
487 WLKEFLRFQEDDSSTSKEKKESYGKQLLHSVQDSQFVHSIKDSGALP 536
    ||||| .|.|| ||
548 WLKEF.....NTAKKPSKKILTPA..... 566

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# Gap (Present Application SEQ ID NO 1 versus Duvick SEQID NO 3)

GAP of: Present application from: 1 to: 1683

readseq-22542\_tmp\_1 1683 bp

to: DUVICK from: 1 to: 1931

readseq-58640\_tmp\_1 1931 bp

Symbol comparison table: /applications/gcg/share/matrix/nwsgapdna.cmp  
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Length Weight:	3	Average Mismatch:	0.000
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Ratio:	4.904	Gaps:	7
Percent Similarity:	52.057	Percent Identity:	52.057

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x May 16, 2008 19:08 ..

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4 gcacatcttcaaagaacatttctactgagatgtcaaaaggtagagctag 53
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 caaaatggagtcgaattgttgagcccttcggaatccctcgaagggactg 250
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54 ctttccaaaaggctttctctttggaactgcttcatcttctatcagtag 103
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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301 aagggtgcttggaaacgaagatggaaaggggaaagcaattgggatcacttc 350
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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204 cgttgatttctaccatcgttacaaggagatattaagagaatgaaggata 253
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254 taaacatggattcgtttcgggctttccattgcttggccacgagttctaact 303
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601 ttttccactgggatgctcctcaagcactagaaagagaagtacggcggtatc 650  
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651 ttagataagactcagaagaggattgtaaatgattacaaaacttcgctaa 700  
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1198 aacatcatcgacatctcaccaaaatactcgctgttctcaacactgacgac 1247  
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1248 gccatcgctagtcaagaaacgatatggcctgacgggaaaccatttgggtcc 1297  
1092 acaaggaggaatcaagatggaatttcacatataccacaggaactcaaaaaa 1141

[illegible]

# GAP (Present Application SEQ ID NO 2 versus Duvick SEQ ID NO 4)

GAP of: Present Application from: 1 to: 560

readseq-8408\_tmp\_1 560 bp

to: DUVICK from: 1 to: 563

readseq-6249\_tmp\_1 563 bp

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Length Weight:	2	Average Mismatch:	-2.248

Quality:	1138	Length:	621
Ratio:	2.032	Gaps:	6
Percent Similarity:	54.582	Percent Identity:	45.418

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x May 16, 2008 18:54 ..

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44 QQSVNDHFSNRFFPHRISDSSDGNVAVDPHYHRYKEDIKRMKDINMDSFRLS 93
      |:| |||| . | || | | . : . | || | : : :| : .| :|
100 GESNWDHFCNHFPERIMDSNADIGANSYHMYKTDVRLCLKEMGMDAYRFS 149
      .
94 IAWPRVLPYGKRDRGVSEEGIKFYNDVIDELLANEITPLVTIFHWDIPQD 143
      |.||||:| | : | :.:|| :| .|. | | | | |||||:| |
150 ISWPRILPKGTVEGGINQDGDIDYKRLINLLENGIEPYVTIFHWDVPQA 199
      .
144 LEDEYGGFL...SEQIIDDFRDYASLCFERFGDRVSLWCTMNEPWWYSVA 190
      ||:||||| ..|:|:|:| .|:| ||| | | ||| :
200 LEEKYGGFLDKTQKRIVNDYKNFAKVCDFDNFGDKVKVNLWTFNEPQTFTSF 249
      .
191 GYDTRKAPGRCSKYVNGASVAGMSGYEAIVSHNMLLAHAEAIVEVFRKC 240
      | | | | | | | . . | | | | | | | | | | | : : |
250 SYGTGVFAPGRCSPLGDCAIPTGNSLVEPYIAGHNILLAHAEAVDLYNKY 299
      .
241 DHIKNQIQIGIAHNPLWYEPYDPSDDPDVEGCNRAMDFMLGWHQHPTACGD 290
      .||:|:| : : | | | : : | .| | | | | |
300 YKGENGRIGLAFDVMGRVPYGTSTFLDE.QAKERSMDINLGWFLEPVVRGD 348
      .
291 YPETMKKSVGDRLPSTPEQSKKLIGSCDYVGINYYSSLFVKSIKHVDPT 340
      || .| : : ||| | . .|:| | . .|||||:| :| |
349 YPFSMRSLARERLPPFSDKQOEKLVGSYNMLGINYYTSTIFSKHIDISPKY 398
      .
341 QPTWRTDQGVDMWMT.NIDGKQIAKGGSEWSTFYPTGLRNILKYVKKTY 389
      . | | | . | ||| | . | : | | | :| | . | |
```



```

399 SPVLNTDDAYASQETYGPDGKPIGPPMGNPWIIYYPEGLKDILMIMKNKY 448
      .
      .
      .
390 GNPPILITENGYGEVARQSQSLMYNPSIDTERLEYIEGHIHAIHQAIHE 439
      .
      .
      .
449 GNPPITYITENGIGDVTKEKPLPMEALNDYKRLDYIQRHISTLKESI.D 497
      .
      .
      .
440 DGVVRVBGYVWSLLDNFEWNSGYGVRYGLYYIDYKDGLRRYPKMSALWLK 489
      .
      .
      .
498 LGANVHGYFAWSLLDNFEWYAGYTERYGIVYVDRKNNYTRYMKESAKWLK 547
      .
      .
      .
490 EFLEFDQEDDSSTSKKEEKESYGKQLLSVQDSQFVHSIKDSGALPAVL 539
      .
      .
      .
548 EF.....NTAKKPSKKIITPA..... 563
      .
      .
      .

```

# BestFit (Present Application SEQ ID NO 1 versus Duvick SEQ ID NO 1)

BESTFIT of: Present Application from: 1 to: 1683

readseq-5573\_tmp\_1 1683 bp

to: DUVICK from: 1 to: 1931

readseq-46685\_tmp\_1 1931 bp

Symbol comparison table: /applications/gcg/share/matrix/swgapdna.cmp  
CompCheck: 2335

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	-9.000
Quality:	1138	Length:	1437
Ratio:	0.807	Gaps:	12
Percent Similarity:	54.500	Percent Identity:	54.500

Match display thresholds for the alignment(s):

| = IDENTITY  
: = 5  
. = 1

28084.seq1.fas x 28084.seq2.fas May 16, 2008 19:01 ..

```
64 ggctttctcttggaaactgcttcattcttatcagtagcgaaggagcagt 113
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
272 gaacttcaccttcggtgccgccacttcagcgtaccaaattgaagggtgctg 321
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
114 gaatgaaggtgcgagaggacaaagcgtgtgggatcatttctccaacaggt 163
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
322 gaatgaagatggaaaggggaaagcaactgggatcacttctgccacaatc 371
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
164 ttctcacagaatcagtgattctagcgacggaacggttgccgttgatttc 213
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
372 atccggaaggaatactggacgggagcaattcagacattggagcgaattcg 421
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
214 taccatcggttacaaggaagatattaagagaatgaaggatataaacatgga 263
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
422 tatcatatgtacaaaacggacgtcagattgctcaaggaaatgggcatgga 471
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
264 ttcgtttcggcttttcattgcttggccacgagttctaccttatggcaaaa 313
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
472 cgcataataggttctctatctcttggcccaagaatactgccgaagggaacca 521
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
314 gggatagaggagtttagtgaagaaggaaattaagttttacaatgatgttatt 363
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
522 aagaaggaggtattaaacctgatggcatcaagtactacagaaacctcatc 571
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
364 gatgaactcttagccaatgaaatcactcctcttggttactatctttcattg 413
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
572 aacttggtgctggaaaacggcatagagccatagtgaacaattttccactg 621
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
414 ggacataccacaggatcttgaagatgaatacggcggttttc...taagc 459
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
622 ggatgtacctcaagcactagaagagaagtacggcggttctctagataaga 671
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
460 g.....agcagattatagatgacttcagagactatgcgagtcctctgcttc 504
```

| | | | | | | | | | | | | | | | | | | | | |  
 672 gtcataagagcatgttagaagattacacctacttcgctaaggtgtgcttt 721  
 | | | | | | | | | | | | | | | | | | | | | |  
 505 gagagatttggggacagagttagtctgtggtgcacaatgaatgagccgtg 554  
 | | | | | | | | | | | | | | | | | | | | | |  
 722 gataacttcgcgacagaaggtgaagaattggtgacctttaatgagcccca 771  
 | | | | | | | | | | | | | | | | | | | | | |  
 555 ggtctacagtgtcgcggtgtatgacacaggaaggaaagcggagacggt 604  
 | | | | | | | | | | | | | | | | | | | | | |  
 772 gacatttacttctcttctctacggaactgggtcttggcccaggtcggt 821  
 | | | | | | | | | | | | | | | | | | | | | |  
 605 gctccaagtattgttaattggcgctagtgtgtggaatgtcgggatacgag 654  
 | | | | | | | | | | | | | | | | | | | | | |  
 822 gctcacctggactagactgtgcctaccacactgggaattcactcgtcgag 871  
 | | | | | | | | | | | | | | | | | | | | | |  
 655 gcataatattgtgagccataaacatgcttctagcgacgcagaaagcagtgga 704  
 | | | | | | | | | | | | | | | | | | | | | |  
 872 ccttacctgctggccataaacattctcctagcccacgctgaggtgttga 921  
 | | | | | | | | | | | | | | | | | | | | | |  
 705 agtgttttagaaaaatgtgaccatattaaaaacggacaaaattgggattgcgc 754  
 | | | | | | | | | | | | | | | | | | | | | |  
 922 tctttacaacaagcattacaagcgcgacgacacccgcataaggcttgcgt 971  
 | | | | | | | | | | | | | | | | | | | | | |  
 755 ataatcoacttttggtacgagccatattgatccgagtgatccagat...gat 801  
 | | | | | | | | | | | | | | | | | | | | | |  
 972 ttgacgtaatgggtcggtgtgccatacggaacatcggttctggataaacag 1021  
 | | | | | | | | | | | | | | | | | | | | | |  
 802 gtcgaaaggtgtaatcgagctatggacttcatgcttgggttggcatcagca 851  
 | | | | | | | | | | | | | | | | | | | | | |  
 1022 gcggaag.....aaaggtcatgggacatcaacctaggatggttcttaga 1065  
 | | | | | | | | | | | | | | | | | | | | | |  
 852 tccgactgcttgggagactatccagaacgatgaagaaatcagttggag 901  
 | | | | | | | | | | | | | | | | | | | | | |  
 1066 ggcagtggttcgtggtgactacccttctccatgagatcattggctaggg 1115  
 | | | | | | | | | | | | | | | | | | | | | |  
 902 atagattaccgagttttacaccagaacaatctaagaaacttataggctct 951  
 | | | | | | | | | | | | | | | | | | | | | |  
 1116 aacgactacccttcttcaaggacgagcagaaggagaagctcgccggttcc 1165  
 | | | | | | | | | | | | | | | | | | | | | |  
 952 tgcgattacgttgggtataaactactatagctcgcttctcgtgaagatgat 1001  
 | | | | | | | | | | | | | | | | | | | | | |  
 1166 tataacatgttggggttaaactactacacctcacggttctccaa..... 1209  
 | | | | | | | | | | | | | | | | | | | | | |  
 1002 caaacacgtggatcctacgcaacctact.....tggagaactgacca 1043  
 | | | | | | | | | | | | | | | | | | | | | |  
 1210 .aaacatcgacatctcac.caaactactcaactgtgctcaacactgaaga 1257  
 | | | | | | | | | | | | | | | | | | | | | |  
 1044 aggcggttgattg...gatgaaaaccaacatagatgggaaacaaatagca 1089  
 | | | | | | | | | | | | | | | | | | | | | |  
 1258 cgcctacgccaagtcaagaagttacggggcct.gacgggaagcccoattggt 1306  
 | | | | | | | | | | | | | | | | | | | | | |  
 1090 aaacaaggaggatcagagtggagtttcacatattccaacaggactcagaaa 1139  
 | | | | | | | | | | | | | | | | | | | | | |  
 1307 cctcctatgggaaatccatggatctacatgtaccctgagggcttgaagga 1356  
 | | | | | | | | | | | | | | | | | | | | | |  
 1140 cattttgaagtattgtgaaaaaaacttatggcaatcctcccattctcataa 1189  
 | | | | | | | | | | | | | | | | | | | | | |  
 1357 tctccttatgataatgaagaacaaatcgggaacccacatctacatca 1406  
 | | | | | | | | | | | | | | | | | | | | | |  
 1190 ctgaaaacgggtattggtgaagtag...cggaacagagtcagagttcttat 1236  
 | | | | | | | | | | | | | | | | | | | | | |  
 1407 ccgagaacgggaatcggggatgttgataccaagagacac...ctctaccc 1453

```

1237 atgtacaatccttcaatcgacacagagagattggagtagattgaaggaca 1286
    ||| | | | | | | | | | | | | | | | | | | | | |
1454 atggaggctgccttaaatgactacaaaaggctagattacatccagcgcca 1503
    .
1287 tatccacgctattcatcaagccatccatgaagatggagtagagtggaag 1336
    ||| | | | | | | | | | | | | | | | | | | | | |
1504 catcgctactcttaaggaatcaat...agacttgggatcaaatgtgcaag 1550
    .
1337 gtattacgtatggctcattgctagataaacttcgagtggaaacagtggatat 1386
    | | | | | | | | | | | | | | | | | | | | | |
1551 gctacttcgcttggctctctgctggacaactttgaatggttgcccggcttc 1600
    .
1387 ggtgtgagatatggtttatattacattgattacaaagatgggcttagacg 1436
    | | | | | | | | | | | | | | | | | | | | | |
1601 accgaacgttatggcattgtctacgtcgaccgcaacaataactgcacgcg 1650
    .
1437 ataccgaaaaatgtcggcggttatggttgaaagagttc 1473
    ||| ||| ||| || | ||||| ||||| |||||
1651 ctacatgaaggagctcgccaagtggttgaaagagttc 1687

```

# BestFit (Present Application SEQ ID NO 2 versus Duvick SEQ ID NO 2)

BESTFIT of: Present Application from: 1 to: 560

readseq-27229\_tmp\_1 560 bp

to: DUVICK from: 1 to: 566

readseq-64774\_tmp\_1 566 bp

Symbol comparison table: /applications/gcg/share/matrix/blosum62.cmp  
Compcheck: 1102

Gap Weight:	8	Average Match:	2.778
Length Weight:	2	Average Mismatch:	-2.248

Quality:	1094	Length:	492
Ratio:	2.242	Gaps:	5
Percent Similarity:	53.814	Percent Identity:	44.536

Match display thresholds for the alignment(s):

```
| = IDENTITY
: = 2
. = 1
```

25165.seq1.fas x 25165.seq2.fas May 16, 2008 18:56 ..

```

4  LQRTFPTEMSKGRASFPKGFLEGTASSSYQYEGAVNEGARGQSVWDHFSN 53
   | . | . . | | | | | . | | | | | : | | | | |
64  VQMLSPSEIPQ.RDWFPDFTFGAATSAYQIEGAWNEDGKGESNWDHFCH 112
   | | | | . : . | | | : : : . | : | | . | | | |
54  RFPHRISDSSDGNVAVDFYHRYKEDIKRMKDINMDSFRLSIAMPRVLPYG 103
   | | | | . : . | | | : : : . | : | | . | | | |
113 NHPERILDGNSNDIGANSYHMYKTDVRLKEMGMDAYRFSISWPRILPKG 162
   | | | | . : . | | | : : : . | : | | . | | | |
104 KDRGVSEBGIKFYNDVIDELLANEITPLVTIFHWDIPODLEDEYGGFLS 153
   : : | : : | | : | . | | | | | | | | | | | | | |
163 TKEGGINPDGIKYRNLINLLENGIEPYVTIFHWDVPOALEEKYGGFLD 212
   | | | | . : . | | | : : : . | : | | . | | | |
154 ...BQIIDDFRDYASLCFERFGDRVSLWCTMNEPWWVYSVAGYDTGRKAPG 200
   | : | : | : | : | | | | | | | | | | | | | |
213 KSHKSIVEDYTYFAKVCFDNPQDKVKNWLTFNEPOTFTSFYSYGTGVFAPG 262
   | | | | . : . | | | : : : . | : | | . | | | |
201 RCSKYVNGASVAGMSGYRAYIVSHNMLLAHAEAIVEFRPKCDHIKNGOIGI 250
   | | | | . : . | | | : : : . | : | | . | | | |
263 RCSPLGDCAYPTGNSLVEPYTAGHNILLAHABAVDLYNKHYKRDDTRIGL 312
   | | | | . : . | | | : : : . | : | | . | | | |
251 AHNPLWYEPYDPSDPPDVEGCNRAMDFMLGWHQHPTACGDYPETMKKSVG 300
   | : | : | | | : | : | . | | | | | | | | | :
313 AFDVMGRVPYGTSLDK.QABERSWDINLGWFLEPVVRGDYPPFSMRSLAR 361
   | | | | . : . | | | : : : . | : | | . | | | |
301 DRLPSFTPBQSKKLIGSCDYVGINYYSSLFVKSIKHVDPTOPTWRDQGV 350
   : | | | | | . | | | | : | | | | | | | | | |
362 ERLPFFKDEQKEKLAGSYNMLGLNYTSTRFSKNIDISPNYSPVLNTDDAY 411
   | | | | . : . | | | : : : . | : | | . | | | |
351 DWMKTN.IDGKQIAKQGGSEWSFTYPTGLRNILKYVKKTYGNPPILITEN 399
   | | | | . : . | | | : : : . | : | | . | | | |
412 ASQEVNGPGDKPIGPPMGNPWIYMYPEGLKDLLMIMKNKYGNPFIYITEN 461
   | | | | . : . | | | : : : . | : | | . | | | |
400 GYGEVAEQSQSLYMYNPISIDTERLEYIEGHIHAIHQAIHEDGVRVEGGYYV 449
   | : | : | | | : | | | : | | | : | | | : | | |
```

462 GIGDVTKETPLPMEAAALNDYKRLDYIQRHIATLKESI.DLGSNVQGYFA 510

450 WSLLDNFEWNSGYGVRYGLYYIDYKDGLRRYPKMSALWLKEF 491

|||||||. |: |||: |:| . || | || ||||

511 WSLLDNFEWFAGFTERYGIVYVDRNNNCTRYMKESAKWLKEF 552

# BestFit (Present Application SEQ ID NO 1 versus Duvick SEQ ID NO 3)

BESTFIT of: Present Application from: 1 to: 1683

readseq-56847\_tmp\_1 1683 bp

to: DUVICK from: 1 to: 1931

readseq-29531\_tmp\_1 1931 bp

Symbol comparison table: /applications/gcg/share/matrix/swgapdna.cmp  
CompCheck: 2335

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	-9.000
Quality:	1782	Length:	1433
Ratio:	1.264	Gaps:	8
Percent Similarity:	56.066	Percent Identity:	56.066

Match display thresholds for the alignment(s):

| = IDENTITY  
: = 5  
. = 1

30007.seq1.fas x 30007.seq2.fas May 16, 2008 19:04 ..

```
64 ggctttctctttggaactgcttcatcttcttcatcagtagcgaaggagcagt 113
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
261 gacttcatcttgggtgccgccacttcagcgtaccaaatgaaggtgcttg 310
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
114 gaatgaaggtgcgagaggacaaagcgtgtgggatcatttctccaacaggt 163
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
311 gacgaagatggaaaggggaaagcaattgggatcacttctgccacaatt 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
164 ttctcacagaatcagtgattctagcgaaggaaacgttgccgttgatttc 213
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
361 ttcggaaaggataaatggacgggagcaatgcagacattggagcgaattcg 410
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
214 taccatcgttacaaggaagatattaagagaatgaaggatataaacatgga 263
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
411 taccatatgtacaaaacggatgtcagattgctgaaggaaatgggcatgga 460
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
264 ttcgtttcggctttccattgcttggccacgagttctacottatggcaaaa 313
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
461 cgcataataggttctctatctcttggcctagaatactgcctaaagggaacgg 510
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
314 gggatagaggagtttagtgaagaaggaattaagttttacaatgatgtatt 363
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
511 tcgaaggaggtattaaccaggatggcatcgattactacaaaagggtcatc 560
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
364 gatgaactcttagccaatgaaatcactcctcttggttactatctttcattg 413
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
561 aacttggtgctagagaatggcatagagccatagtgaacaattttccactg 610
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
414 ggacataccacaggatcttgaagatgaatacggcggtttttcta..... 456
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
611 ggatgtccctcaagcactagaagagaagtacggcggtattcttagataaga 660
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
457 ..agcgagcagattatagatgaactcagagactatgcgagttctctgcttc 504
```

661 ct cagaagaggattgtaaatgattacaaaaactcgctaagggtgtgcttc 710  
 505 gagagatttggggacagagtgtgctgtgggtgcacaatgaatgagccgtg 554  
 711 gacaactttggtgacaaggtgaagaattggtgacctttaatgagcccca 760  
 555 ggtctacagtgtcgcgggctatgacacaggaaggaagcgccaggacggt 604  
 761 gacatttacttcatcttctcatggaacggggtcttggccccaggacgat 810  
 605 gctccaagtattgttaatggcgctagtgttctgtggaatgtcgggatacag 654  
 811 gctcacgggactagactgtgccatcccaactgggaattcaactcgtcgaa 860  
 655 gcataatattgtgagccataaacatgcttcttagcgacgcagaaagcagtgga 704  
 861 ccttacattgtcgtggccacacaacatctcttagccacgctgaggctgttga 910  
 705 agtgttttagaaaaatgtgaccatattaaaaacggacaaaattgggattgcgc 754  
 911 tctttacaacaagtattacaagggcgagaacggccgcataggtcttgat 960  
 755 ataatacacttttggtacgagccatgatccgagtgatccagatg...at 801  
 961 ttgatgtaatgggtcgtgtgcccatacggaacatcatttctagatgaacag 1010  
 802 gtcgaaggatgtaatcgagctatggacttcatgcttgggttggcatcagca 851  
 1011 gccaaag.....aaagggtccatggacattaacctaggatggttcttggga 1054  
 852 tccgactgcttggtagactatccagaaacgatgaagaaatcagttggag 901  
 1055 gcctgtggttcgtggtgactaccctctctcaatgagatcgttagcgaggg 1104  
 902 atagattaccgagttttacaccagaacaactaagaaacttataggtctct 951  
 1105 aacgactaccctcttctcagtgacaaacagcaagagaagcttggggatcc 1154  
 952 tgcgattacgttgggtataaaactactatagctcgcttttctgtaagatgat 1001  
 1155 tataacatgttgggaataaaactactacacctcaatattctccaacatcat 1204  
 1002 caaacacgtggatcctacgcaa.....cctacttggaactgaccaa 1044  
 1205 cga.....catctcaccaaaatactcgctgttctcaacactgacgac 1247  
 1045 ggcggttgattggatgaaaaccaa...catagatgggaaacaaatagcaaa 1091  
 1248 gcctacgctagtcaagaaacgtatgggcctgacgggaacccattggtcc 1297  
 1092 acaaggaggatcagagtggagtttccatattccaacaggactcagaacaa 1141  
 1298 tcctatgggaaatcgtggatctacttataccagaaggctcaaaagata 1347  
 1142 ttttgaagtatgtgaaaaaaacttatggcaatcctccattctcataact 1191  
 1348 tccttatgatcatgaagaacaaatattggaacccacctatctacatcact 1397  
 1192 gaaaacgggtatggtgaagttagcggaacagagtcagagtcctttatatgta 1241  
 1398 gagaacggaatcggggatgttgatacaaaggagaaacctctaccatgga 1447



```

1242 caatccttcaatcgacacagagagattggagtacattgaaggacatatcc 1291
    | | | | | | | | | | | | | | | | | | | | | |
1448 ggctgccttaaatgactacaaaaggctagattacatccagcgccacatct 1497
    .
1292 acgctattcatcaagccatccat.gaagatggagtaagagtggaaggtta 1340
    | | | | | | | | | | | | | | | | | | | | | |
1498 caact....ctcaaggagtcaatagacttgggagcaaatgtgcatggcta 1543
    .
1341 ttacgtatggtcattgctagataacttcgagtggaacagtggtatggtg 1390
    | | | | | | | | | | | | | | | | | | | | | |
1544 ctctgcttgggtctctgctggataactttgaatgggtacgcccgtacaccg 1593
    .
1391 tgagatatggtttatattacattgattacaaagatgggcttagacgatac 1440
    | | | | | | | | | | | | | | | | | | | | | |
1594 aacgttatggcattgtctacgtcgaccgcaaaaaatactacacgcgctac 1643
    .
1441 ccgaaaatgtcggcgttatggttgaaagagttc 1473
    | | | | | | | | | | | | | | | | | | | | | |
1644 atgaaggagtcagccaagtggttaaaagagttc 1676

```

# BestFit (Present Application SEQ ID NO 2 versus Duvick SEQ ID NO 4)

BESTFIT of: Present Application from: 1 to: 560

readseq-44782\_tmp\_1 560 bp

to: DUVICK from: 1 to: 563

readseq-7768\_tmp\_1 563 bp

Symbol comparison table: /applications/gcg/share/matrix/blosum62.cmp  
CompCheck: 1102

Gap Weight:	8	Average Match:	2.778
Length Weight:	2	Average Mismatch:	-2.248
Quality:	1152	Length:	492
Ratio:	2.361	Gaps:	5
Percent Similarity:	55.464	Percent Identity:	45.979

Match display thresholds for the alignment(s):

| = IDENTITY  
: = 2  
. = 1

26267.seq1.fas x 26267.seq2.fas May 16, 2008 18:58 ..

```

      .
4  LORTFPTEMSKGRASFPKGFPLGTTASSSYQYEGAVNEGARGQSVWDHFSN 53
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
61 VQLLSPESEIPR.RDWFPSPDFPGAATSAYQIEGAWNEDGKGESNWDHFC 109
      .
      .
54 RFPHRISDSSDGNVAVDYFYHRYKEDIKMKDINMDSFRLSIAPRVLPY 103
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
110 NPPERIMDGSNADIGANSYHMYKTDVRLLEKMGMDAYRFSISWPRILPK 159
      .
      .
104 KRDRGVSEEGIKFYNDVIDELLANEITPLVTIPHWDIPODLEDEYGGFL 152
      : | : : | | : | . | | | | | | | | | | | | | | | | |
      : | : : | | : | . | | | | | | | | | | | | | | | | |
160 TVEGGINQDGIDYKRLINLLENGIEPYVTIPHWDPQALEEKYGGFLD 209
      .
      .
153 ..SEQIIDDFRDYASLCPERFGDRVSLWCTMNEPWWYSVAGYDTGRKAP 200
      ..| : | : : | | | : | | : | | | | | | | | | | | |
      ..| : | : : | | | : | | : | | | | | | | | | | | |
210 KTQKRIVNDYKNPAKVCDFNFGDKVKKNWLTPEPQITFSFSYGTGVFAP 259
      .
      .
201 RCSKYVNGASVAGMSGYEAYIVSHNMLLAHAEAVEVFRKCDHIKNGOIG 250
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
260 RCSPLDCAIPTGNSLVEPYIAGHNILLAHAEAVDLYNKYYKGENGRIGL 309
      .
      .
251 AHNPLWYEPYDPSDDVEGCNRAMDFMLGWHQHPTACGDYPTMKKSVG 300
      | : : | | | : | : | | | | | | | | | | | | | | | |
      | : : | | | : | : | | | | | | | | | | | | | | | |
310 AFDVMGRVPYGTSLFDE.QAKERSMDINLGFLEPVVRGDYPPFMRSLAR 358
      .
      .
301 DRLPSPTPEQSKKLIGSCDYVGINYSSLFVKSIXHVDPTQPTWRTDQGV 350
      : | | | | . | : | | | . | | | | | | : | | | | | | |
      : | | | | . | : | | | . | | | | | | : | | | | | | |
359 ERLPFFSDKQOEKLVGSYNMLGINYYTSPISKHIDISPKYSPVLNTDDAY 408
      .
      .
351 DWMKT.NIDGKQIAKQGGSEWSPTYPTGLRNILKYVKKTYGNPPILIT 399
      . | | | | | | | | | | | | | | | | | | | | | | | | | |
      . | | | | | | | | | | | | | | | | | | | | | | | | | |
409 ASQETYGPDGKPIGPFMGNFWIYLYPEGLDKDILMIMKNKYGNPPYITEN 458
      .
      .
400 GYGEVARQSQSLMYNPSIDTERLEYIEGHIHAIHQAIHEDGVRVEGYV 449
      | : | . . | | | . | : | : | | | : : . | : | | : |
```

459 GIGDVDTEKPLPMEAAALNDYKRLDYIQRHISTLKESI.DLGANVHGYPFA 507

450 WSLLDNFEWNSGYGVRYGLYYIDYKDGLRRYPKMSALWLKEF 491

||||| .|| ||: |:| |. || || |||

508 WSLLDNFEWYAGYTERYGIVYVDRKNNYTRYMKESAKWLKEF 549